

RAW SEQUENCE LISTING

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Application Serial Number: 10/677, 983

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RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/677,983

TIME: 09:24:30

Input Set : N:\Crf3\RULE60\10677983.raw.txt

Output Set: N:\CRF4\10182004\J677983.raw

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1 <110> APPLICANT: FELDER, ROBIN A.
2   JOSE, PEDRO
3 <120> TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
4   HYPERTENSION
5 <130> FILE REFERENCE: FELDER 3.9-001 CONT
6 <140> CURRENT APPLICATION NUMBER: US/10/677,983
7 <141> CURRENT FILING DATE: 2003-10-02
8 <150> PRIOR APPLICATION NUMBER: US/09/614,748
9 <151> PRIOR FILING DATE: 2000-07-12
10 <150> PRIOR APPLICATION NUMBER: PCT/US99/00663
11 <151> PRIOR FILING DATE: 1999-01-12
12 <150> PRIOR APPLICATION NUMBER: 60/071,199
13 <151> PRIOR FILING DATE: 1998-01-12
14 <150> PRIOR APPLICATION NUMBER: 60/098,279
15 <151> PRIOR FILING DATE: 1998-08-28
16 <160> NUMBER OF SEQ ID NOS: 34
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 578
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
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27       20           25           30
28   Ile Leu Thr Leu Pro Pro Val Ser Gln Cys Ser Glu Leu Arg His Ser
29       35           40           45
30   Ile Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
31       50           55           60
32   Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Thr Leu Lys Arg His
33       65           70           75           80
34   Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
35       85           90           95
36   Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
37       100          105          110
38   Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu
39       115          120          125
40   Cys Arg Leu Gly Leu Lys Glu Glu Asn Pro Ser Lys Lys Ala Phe Glu
41       130          135          140
42   Glu Cys Thr Arg Val Ala His Asn Tyr Leu Arg Gly Glu Pro Phe Glu
43       145          150          155          160
44   Glu Tyr Gln Glu Ser Ser Tyr Phe Ser Gln Phe Leu Gln Trp Lys Trp

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45				165				170				175
46	Leu	Glu	Arg	Gln	Pro	Val	Thr	Lys	Asn	Thr	Phe	Arg
47				180				185				190
48	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Glu	Val	Cys	Ala	Cys
49			195					200				205
50	Thr	Gly	Lys	Met	Tyr	Ala	Cys	Lys	Lys	Leu	Gln	Lys
51		210					215				220	
52	Lys	Arg	Lys	Gly	Glu	Ala	Met	Ala	Leu	Asn	Glu	Lys
53		225			230					235		240
54	Lys	Val	Gln	Ser	Arg	Phe	Val	Val	Ser	Leu	Ala	Tyr
55				245				250				255
56	Lys	Asp	Ala	Leu	Cys	Leu	Val	Leu	Thr	Ile	Met	Asn
57			260					265				270
58	Lys	Phe	His	Ile	Tyr	Asn	Leu	Gly	Asn	Pro	Gly	Phe
59			275					280				285
60	Ala	Val	Phe	Tyr	Ala	Ala	Glu	Leu	Cys	Cys	Gly	Leu
61		290					295				300	
62	Arg	Glu	Arg	Ile	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu
63		305				310					315	
64	Asp	Asp	Arg	Gly	His	Ile	Arg	Ile	Ser	Asp	Leu	Gly
65				325				330				335
66	Ile	Pro	Glu	Gly	Gln	Arg	Val	Arg	Gly	Arg	Val	Gly
67			340					345				350
68	Met	Ala	Pro	Glu	Val	Val	Asn	Asn	Glu	Lys	Tyr	Thr
69			355					360				365
70	Trp	Trp	Gly	Leu	Gly	Cys	Leu	Ile	Tyr	Glu	Met	Ile
71		370					375				380	
72	Pro	Phe	Lys	Lys	Tyr	Lys	Glu	Lys	Val	Lys	Trp	Glu
73		385				390				395		400
74	Arg	Ile	Lys	Asn	Asp	Thr	Glu	Glu	Tyr	Ser	Glu	Lys
75				405				410				415
76	Ala	Lys	Ser	Ile	Cys	Arg	Met	Leu	Leu	Thr	Lys	Asn
77			420					425				430
78	Leu	Gly	Cys	Arg	Gly	Glu	Gly	Ala	Ala	Gly	Val	Lys
79		435					440				445	
80	Phe	Lys	Asp	Ile	Asn	Phe	Arg	Arg	Leu	Glu	Ala	Asn
81		450				455				460		
82	Pro	Phe	Cys	Pro	Asp	Pro	His	Ala	Val	Tyr	Cys	Lys
83		465				470				475		480
84	Ile	Glu	Gln	Phe	Ser	Ala	Val	Lys	Gly	Ile	Tyr	Leu
85				485				490				495
86	Glu	Asp	Phe	Tyr	Ala	Arg	Phe	Ala	Thr	Gly	Cys	Val
87			500					505				510
88	Gln	Asn	Glu	Met	Ile	Glu	Ser	Gly	Cys	Phe	Lys	Asp
89			515					520				525
90	Glu	Ser	Glu	Glu	Ala	Leu	Pro	Leu	Asp	Leu	Asp	Lys
91		530					535				540	
92	Pro	Val	Ser	Arg	Pro	Asn	Arg	Gly	Phe	Phe	Tyr	Arg
93		545				550				555		560

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99 <211> LENGTH: 546
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
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104              1              5              10              15
105      Gln Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
106              20              25              30
107      Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Ile Leu Lys Arg His
108              35              40              45
109      Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
110              50              55              60
111      Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
112              65              70              75              80
113      Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu
114              85              90              95
115      Cys Arg Leu Gly Leu Lys Glu Glu Asn Pro Ser Lys Lys Ala Phe Glu
116              100             105             110
117      Glu Cys Thr Arg Val Ala His Asn Tyr Leu Arg Gly Glu Pro Phe Glu
118              115             120             125
119      Glu Tyr Gln Glu Ser Ser Tyr Phe Ser Gln Phe Leu Gln Trp Lys Trp
120              130             135             140
121      Leu Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg His Tyr Arg Val
122              145             150             155             160
123      Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala
124              165             170             175
125      Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Gln Lys Lys Arg Ile Lys
126              180             185             190
127      Lys Arg Lys Gly Glu Ala Met Ala Leu Asn Glu Lys Arg Ile Leu Glu
128              195             200             205
129      Lys Val Gln Ser Arg Phe Val Val Ser Leu Ala Tyr Ala Tyr Glu Thr
130              210             215             220
131      Lys Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu
132              225             230             235             240
133      Lys Phe His Ile Tyr Asn Leu Gly Asn Pro Gly Phe Asp Glu Gln Arg
134              245             250             255
135      Ala Val Phe Tyr Ala Ala Glu Leu Cys Cys Gly Leu Glu Asp Leu Gln
136              260             265             270
137      Arg Glu Arg Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu
138              275             280             285
139      Asp Asp Arg Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Thr Glu
140              290             295             300
141      Ile Pro Glu Gly Gln Arg Val Arg Gly Arg Val Gly Thr Val Gly Tyr
142              305             310             315             320
143      Met Ala Pro Glu Val Val Asn Asn Glu Lys Tyr Thr Phe Ser Pro Asp

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144          325          330          335
145 Trp Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Gln Gly His Ser
146          340          345          350
147 Pro Phe Lys Lys Tyr Lys Glu Lys Val Lys Trp Glu Glu Val Asp Gln
148          355          360          365
149 Arg Ile Lys Asn Asp Thr Glu Glu Tyr Ser Glu Lys Phe Ser Glu Asp
150          370          375          380
151 Ala Lys Ser Ile Cys Arg Met Leu Leu Thr Lys Asn Pro Ser Lys Arg
152          385          390          395          400
153 Leu Gly Cys Arg Gly Glu Gly Ala Ala Gly Val Lys Gln His Pro Val
154          405          410          415
155 Phe Lys Asp Ile Asn Phe Arg Arg Leu Glu Ala Asn Met Leu Glu Pro
156          420          425          430
157 Pro Phe Cys Pro Asp Pro His Ala Val Tyr Cys Lys Asp Val Leu Asp
158          435          440          445
159 Ile Glu Gln Phe Ser Ala Val Lys Gly Ile Tyr Leu Asp Thr Ala Asp
160          450          455          460
161 Glu Asp Phe Tyr Ala Arg Phe Ala Thr Gly Cys Val Ser Ile Pro Trp
162          465          470          475          480
163 Gln Asn Glu Met Ile Glu Ser Gly Cys Phe Lys Asp Ile Asn Lys Ser
164          485          490          495
165 Glu Ser Glu Glu Ala Leu Pro Leu Asp Leu Asp Lys Asn Ile His Thr
166          500          505          510
167 Pro Val Ser Arg Pro Asn Arg Gly Phe Phe Tyr Arg Leu Phe Arg Arg
168          515          520          525
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175 <211> LENGTH: 532
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
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182 20 25 30
183 Ile Leu Thr Leu Pro Pro Val Ser Gln Cys Ser Glu Leu Arg His Ser
184 35 40 45
185 Ile Glu Lys Asp Tyr Ser Ser Leu Cys Asp Lys Gln Pro Ile Gly Arg
186 50 55 60
187 Arg Leu Phe Arg Gln Phe Cys Asp Thr Lys Pro Ile Leu Lys Arg His
188 65 70 75 80
189 Ile Glu Phe Leu Asp Ala Val Ala Glu Tyr Glu Val Ala Asp Asp Glu
190 85 90 95
191 Asp Arg Ser Asp Cys Gly Leu Ser Ile Leu Asp Arg Phe Phe Asn Asp
192 100 105 110
193 Lys Leu Ala Ala Pro Leu Pro Glu Ile Pro Pro Asp Val Val Thr Glu

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194																
195	Cys	Arg	Leu	Gly	Leu	Lys	Glu	Glu	Asn	Pro	Ser	Lys	Lys	Ala	Phe	Glu
196			130					135					140			
197	Glu	Cys	Thr	Arg	Val	Ala	His	Asn	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	Glu
198							150					155				160
199	Glu	Tyr	Gln	Glu	Ser	Ser	Tyr	Phe	Ser	Gln	Phe	Leu	Gln	Trp	Lys	Trp
200						165					170					175
201	Leu	Glu	Arg	Gln	Pro	Val	Ile	Lys	Asn	Thr	Phe	Arg	His	Tyr	Arg	Val
202						180				185					190	
203	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala
204						195			200				205			
205	Thr	Gly	Lys	Met	Tyr	Ala	Cys	Lys	Lys	Leu	Gln	Lys	Lys	Arg	Ile	Lys
206						210			215				220			
207	Lys	Arg	Lys	Gly	Glu	Ala	Met	Ala	Leu	Asn	Glu	Lys	Arg	Ile	Leu	Glu
208						225						235				240
209	Lys	Val	Gln	Ser	Arg	Phe	Val	Val	Ser	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr
210						245					250					255
211	Lys	Asp	Ala	Leu	Cys	Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu
212						260				265					270	
213	Lys	Phe	His	Ile	Tyr	Asn	Leu	Gly	Asn	Pro	Gly	Phe	Asp	Glu	Gln	Arg
214						275				280				285		
215	Ala	Val	Phe	Tyr	Ala	Ala	Glu	Leu	Cys	Cys	Gly	Leu	Glu	Asp	Leu	Gln
216						290			295				300			
217	Arg	Glu	Arg	Ile	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu
218						305						315				320
219	Asp	Asp	Arg	Gly	His	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Thr	Glu
220						325					330					335
221	Ile	Pro	Glu	Gly	Gln	Arg	Val	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr
222						340				345					350	
223	Met	Ala	Pro	Glu	Val	Val	Asn	Asn	Glu	Lys	Tyr	Thr	Phe	Ser	Pro	Asp
224						355			360					365		
225	Trp	Trp	Gly	Leu	Gly	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Gln	Gly	His	Ser
226						370			375				380			
227	Pro	Phe	Lys	Lys	Tyr	Lys	Glu	Lys	Val	Lys	Trp	Glu	Glu	Val	Asp	Gln
228						385						395				400
229	Arg	Ile	Lys	Asn	Asp	Thr	Glu	Glu	Tyr	Ser	Glu	Lys	Phe	Ser	Glu	Asp
230						405					410					415
231	Ala	Lys	Ser	Ile	Cys	Arg	Met	Leu	Leu	Thr	Lys	Asn	Pro	Ser	Lys	Arg
232						420				425					430	
233	Leu	Gly	Cys	Arg	Gly	Glu	Gly	Ala	Ala	Gly	Val	Lys	Gln	His	Pro	Val
234						435			440			</				

VERIFICATION SUMMARY

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